IN THE CLAIMS:

Claim 1. (Amended) A method for characterizing a genetic profile of a selected chromosome pair, comprising:

forming multiple luminescent hybridization probes to hybridize to a wild-type and a mutant polymorphism at a first polymorphic target site and to a wild-type and a mutant polymorphism at a second polymorphic target site, where the probes for the wild-type polymorphic sites have at least one recognizable luminescent characteristic and the probes for the mutant polymorphic sites have at least a second recognizable luminescent characteristic and where the first and second polymorphic sites are located on the selected chromosome and are linked to a selected genetic characteristic;

forming single stranded DNA at least along segments of DNA forming the chromosome, where the single stranded DNA segments contain the first and second polymorphic sites;

forming probe pairs from the luminescent probes, where each probe pair contains a probe specific to the first polymorphic site and a probe specific to the second polymorphic site;

specifically hybridizing each probe pair in separate solutions of the single stranded DNA and determining the presence or absence of each luminescent hybridization probe in each segment of DNA in each solution to obtain a set of outputs; and

analyzing the set of outputs from the hybridized probes to determine the complete haplotype that characterizes the genetic profile of the selected chromosome pair [rapid haplotyping comprising the steps of:

labeling at least two target sites on a segment of DNA or RNA with separate distinguishable luminescent hybridization probes, where the targets are selected genetic markers; and

detecting the presence or absence of each luminescent hybridization probe on each DNA segment to determine the haplotype of each DNA or RNA segment].